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ORIGINAL RESEARCH

RETRACTED ARTICLE: MiR-29a function as tumor suppressor in cervical cancer by targeting SIRT1 and predict patient prognosis

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Ping Nan[1]
Yugui Niu[2]
Xiuhua Wang[3]
Qiang Li[1]

[1]Department of Gynaecology, Shengli Oil Centre Hospital, Dongying, People's Republic of China; [2]Department of Joint Surgery, Shengli Oil Center Hospital, Dongying, People's Republic of China; [3]Department of Gynecology, Dongying District People's Hospital, Dongying, People's Republic of China

Introduction: Cervical cancer is the second most frequently malignant tumors in females and metastasis is a challenge of the treatment of cervical cancer. MiR-29a is usually low expressed in several tumors and its function in cervical cancer remain unclear.

Patients and methods: The quantitative real-time polymerase chain reaction was employed to assess the expression of miR-29a and the Sirtuin-1 (SIRT1). Cell metastatic ability was assessed using Transwell and Western blot assays. The dual-luciferase reporter assay was performed to verify that miR-29a targeted to the 3'-untranslated region (UTR) of SIRT1 mRNA.

Results: MiR-29a was low expressed in cervical cancer and downregulation of miR-29a was associated with poor outcome. MiR-29a regulated the expression of SIRT1 by targeting to its 3'-UTR of mRNA in HeLa cells. SIRT1 was upregulated in cervical cancer tissues and cells in comparison with the normal tissues and normal cells. Upregulation of SIRT1 predicted worse outcome of cervical cancer patients. MiR-29a was participated in the migration, invasion and epithelial–mesenchymal transition (EMT) in cervical cancer through directly targeting to the 3'-UTR of SIRT1 mRNA. SIRT1 reversed partial roles of miR-29a on metastasis in cervical cancer.

Conclusion: miR-29a suppressed migration, invasion and EMT by directly targeting to SIRT1 in cervical cancer. The newly identified miR-29a/SIRT1 axis provides novel insight to the pathogenesis of cervical cancer.

Keywords: miR-29a, cervical cancer, SIRT1, tumor suppressor, EMT

Introduction

Cervical cancer is the second most frequently malignant tumors in females with more than 260,000 deaths in 2015, according to the WHO datum.[1,2] The metastasis of tumor still occurs, even though the mortality rates of cervical cancer patients reduced due to the early screening programs.[3] However, the metastasis molecular mechanisms of cervical cancer still unclear, thus, it is still urgent to explore newly biomarkers for the metastasis of cervical cancer.

MicroRNAs (miRNAs) were a quantity of short non-coding RNAs that could inhibit the function of target genes through degrading the mRNA or suppressing its translation in post-transcriptional regulation.[4,5] MiR-29a has been reported to be a tumor suppressors and was participated in the proliferation of glioma and lung cancer.[6,7] Xiong et al[8] revealed that miR-29a inhibited the growth and metastasis through targeting BMI1 in melanoma. Similarly, Liu et al[9] validated that miR-29a

Correspondence: Qiang Li
Department of Gynaecology, Shengli Oil Centre Hospital, No. 31 Jinan Road, Dongying District, Dongying District 257000, People's Republic of China
Tel +86 158 8997 7885
Email rllkumf@163.com

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suppressed viability, migration and invasion via TRAF4/Akt Signaling in glioma. Even in endometrial carcinoma, miR-29a impaired the viability and invasion, and induced the apoptosis through targeting TPX2.[10] Thus, we hypothesize that miR-29a may play a role in cervical cancer.

Sirtuin-1 (SIRT1) encodes a member of the sirtuin family of proteins that was a highly conserved histone deacetylases.[11] SIRT1 was overexpressed in several cancers, including breast cancer, colon cancer and gastric cancer.[12] As we know, yeast sirtuin proteins regulate epigenetic gene silencing and suppress recombination of rDNA.[13,14] The neuronal SIRT1 activity plays an important role in regulating energy balance and glucose metabolism, and suppressed reproductive cycles.[15] Borji et al[16] elucidated that knockdown of SIRT1 promoted liver cell viability and lipid accumulation in hepatocytes. Moreover, Gorski et al[17] demonstrated that knockdown of SIRT1 inhibited the growth of cardiomyocytes. Inhibition of SIRT1 increased the activity of the tumor suppressor gene p53 and facilitated the expression of antiproliferative gene p21.[18] In this study, miR-29a regulated the expression of SIRT1 by directly targeting to 3'-UTR of its mRNA in HeLa cells. MiR-29a was participated in the migration, invasion and epithelial–mesenchymal transition (EMT) through targeting SIRT1 in cervical cancer.

Patients and methods

Tumor specimens

Fifty-four patients with cervical cancer who were hospitalized in Shengli oil center hospital were collected during 2016 to 2018, and through surgical operation, we obtained pairs of cervical cancer and corresponding paracancerous tissues. The fresh tissues were stored at −80°C followed by frozen immediately in liquid nitrogen after surgery. All samples received written informed consent from the patients and were approved by the Ethical Committee of Shengli oil center hospital. This study was conducted in accordance with the Declaration of Helsinki.

Cell culture and treatment

A normal cervical immortalized squamous cell line Ect1/E6E7 and a cervical cancer cell line HeLa were obtained from American Type Culture Collection (Rockville, MD, USA). All the cells were cultured in DMEM (Gibco, Grand Island, NY, USA) containing 10% FBS (Gibco, Grand Island, NY, USA) and incubated at 37°C in 5% CO_2 atmosphere.

Cell transfection

MiR-29a mimic or miR-29a inhibitor (Gene Pharma, Shanghai, People's Republic of China) was used to up- or downregulate the intracellular miR-29a levels. HeLa cells with a density of 70% were seeded into 6-well plates. Transfection was carried out using Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA), which was diluted in Opti-MEM medium. Next, we added the mixture to the cells and incubated the cells at 37°C.

RNA extraction and quantitative real-time polymerase chain reaction (qRT-PCR)

Total RNA or miRNA was extracted using TRIzol reagent (Invitrogen) or miRCURY RNA Isolation Kit (Exiqon, Vedbaek, Denmark), which was quantified by a NanoDrop spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA). The first complementary deoxyribonucleic acids (cDNAs) chain was synthesized using the High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems, Foster City, CA, USA). The expression of SIRT1 or miR-29a was calculated using the SYBR PrimeScript miRNA RT-PCR kit or the SYBR PrimeScript miRNA RT-PCR kit (TaKaRa Bio, Otsu, Japan), with glyceraldehyde 3-phosphate dehydrogenase (GAPDH) and U6 as the internal reference. The primers were: miR-29a F: 5'-UAGCACCAUCUGAAAUCGGUUA-3', R: 5'-ACCGUGCUCGACUUUCCGG-3'; U6 F: 5'-CTCGCTTCGGCAGCACATATACT-3', R: 5'-ACGCTTCACGAATTTGCGTGTC-3'; SIRT1 F: 5'-AGTCCTGCTCCTTCCAAAAC-3', R: 5'-CTTCGGTGTAGCCCATTTGT-3';

GAPDH F: 5'-ACAGCAACAGGGTGGTGGAC-3',
R: 5'-TTTGAGGGTGCAGCGAACTT-3'.

Western blotting

Cells were lyse and extracted proteins using radio immunoprecipitation assay buffer containing protease inhibitors (Sigma, St. Louis, MO, USA). After centrifugation at 12,000 rpm for 15 mins, the concentration of total protein was assessed using bicinchoninic acid Protein Assay Kit (Thermo Scientific). We separated the proteins using 10% dodecyl sulfate, SDS-PAGE followed transferred onto polyvinylidene fluoridemembranes (Roche Applied Science, Basel, Switzerland).

After the membrane was blocked by incubating 5% skim milk for 2 hrs at room temperature, it was subsequently incubated with the primary antibodies. The primary antibodies were SIRT1, E-cadherin, N-cadherin and

GAPDH. After incubated with these primary antibodies, the membranes were washed in tris buffered saline-tween (TBST) and then incubated with the secondary horseradish peroxidase-conjugated antibody (1:5000). Visualization was carried out using a Western enhanced chemiluminescence Substrate (Bio-Rad, Hercules, CA, USA).

Transwell assay

Transwell assays without or with Matrigel were utilized to investigate the abilities of migration and invasion in cervical cancer cells. Prior to the experiment, the transwell chambers were placed in 24-well plate. We seeded cell suspension which were suspended in basal DMEM without FBS in the upper chamber, while adding 600 μL DMEM containing 20% FBS to the lower chamber. The migrated or invaded cells were moved to the underside of the membranes. After 48 hrs of culture, removed the cells stayed on the upper surface by using cotton swab, then fixed and stained the cells with methanol and crystal violet. We counted the number of cells that migrated or invaded under a microscope.

Luciferase reporter gene assay

The wild type or mutant type of SIRT1 mRNA 3'UTR was inserted in psiCHECK™2 vector (Promega Corporation, Madison, WI, USA). HeLa cells were co-transfected with miR-29a mimic or mimic NC, and wild type or mutant type vectors using Lipofectamine 2000 (Invitrogen). After 48 hrs of transfection, firefly and Renilla luciferase activity were assessed using a Dual-Luciferase Reporter Assay system (Promega Corporation).

Statistical analysis

Statistical analysis was performed using GraphPad Prism 7 Software (La Jolla, CA, USA). Data are presented as mean ±SD of at least three independent triplicate experiments. The *t*-test was used to analyze the measurement data. Differences between the two groups were analyzed by using the Student's *t*-test. Comparisons between multiple groups were performed using a one-way ANOVA test followed by a post hoc test (least significant difference). Statistically significant difference was considered as $P<0.05$.

Results

Low expression of miR-29a predicted poor prognosis of cervical cancer

The expression of miR-29a was evaluated in 54 pairs of cervical cancer and corresponding paracancerous tissues by RT-qPCR. MiR-29a was downregulated in cervical cancer versus corresponding paracancerous tissues ($P<0.05$) (Figure 1A). Kaplan–Meier method was utilized to assess the relationship between the expression of miR-29a and overall survival, and it elucidated that low expression of miR-29a predicted poor overall survival of cervical cancer patients ($p<0.05$) (Figure 1B).

Moreover, the miR-29a expression was calculated in cervical immortalized squamous cell line Ect1/E6E7 and cervical cancer cell line HeLa. As expected, the expression of miR-29a was lower in HeLa cells than Ect1/E6E7 cells ($P<0.05$) (Figure 1C). The transfection efficiency of transfecting the miR-29a mimic ($P<0.01$) or the miR-29a inhibitor was measured by RT-qPCR in HeLa cells ($P<0.05$) (Figure 1D).

MiR-29a impaired cell metastasis and EMT of HeLa cells

The migratory and invasive abilities were calculated in HeLa cells using Transwell assay. The results elucidated that the miR-29a mimic inhibited the migratory and invasive capacities ($P<0.01$), whereas those were inhibited by miR-29a inhibitor ($P<0.05$) (Figure 2A and B). Western blot results revealed that the miR-29a mimic suppressed the EMT ability by inhibiting the expression of E-cadherin, but improving the expression of N-cadherin. In contrary, the miR-29a inhibitor enhanced the EMT phenomenon of cervical cancer by enhancing the expression of E-cadherin whereas suppressing the expression of N-cadherin (Figure 2C). All the results elucidated miR-29a improved the abilities of metastasis and EMT in HeLa cells.

MiR-29a regulated the expression of SIRT1 through directly binding to the 3'-UTR of its mRNA

TargetScan was conducted to predict the potential target genes of miR-29a, and SIRT1 was discovered as a target of miR-29a. To validate the correlation between miR-29a and SIRT1, the conjectural binding sequences were mutated from ACCACGA to UGGUGCU, and followed we performed the luciferase reporter assay (Figure 3A). Not unexpectedly, the miR-29a mimic suppressed the luciferase activity of wild type SIRT1 3'-UTR, in comparison with the NC mimic ($P<0.05$). However, the luciferase activity of the mutated 3'-UTR of SIRT1 mRNA has no alteration by the miR-29a mimic ($P>0.05$) (Figure 3B).

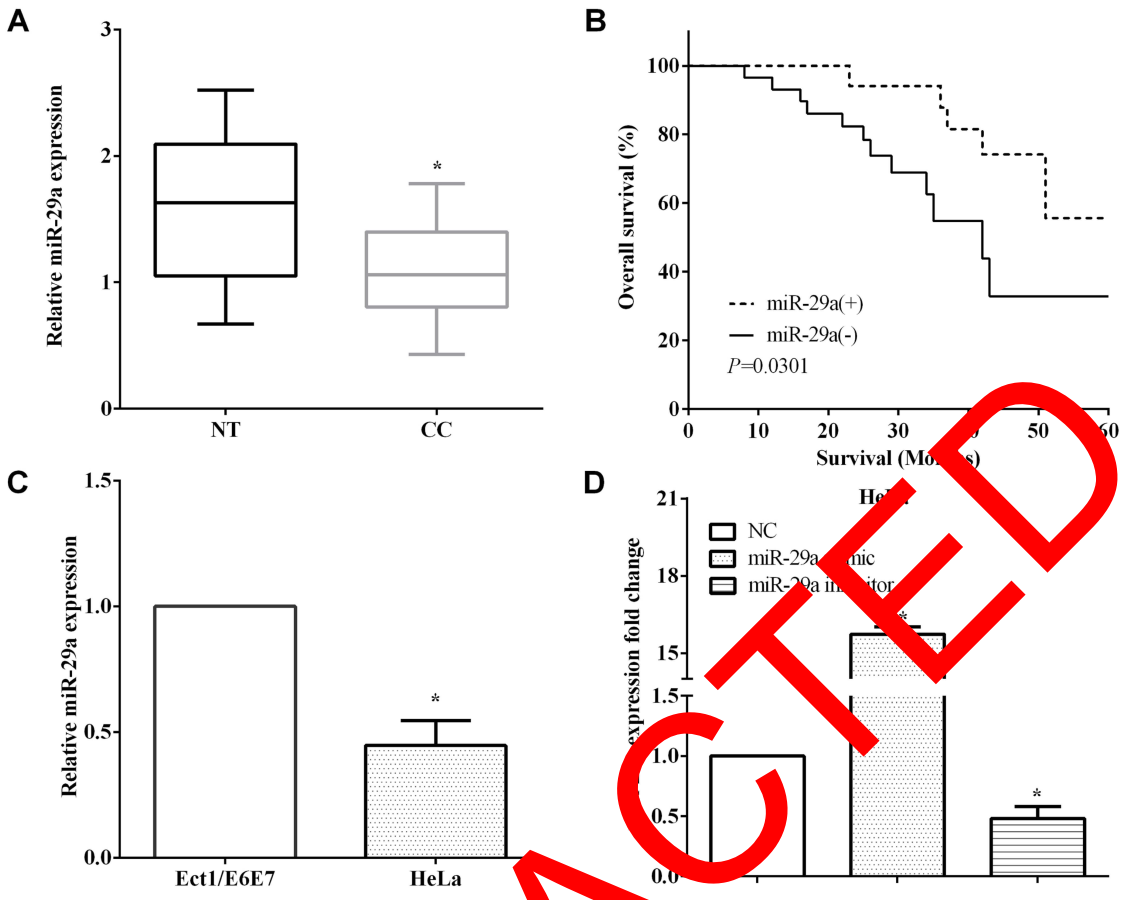

Figure 1 Low expression of miR-29a predicted poor prognosis of cervical can[illegible]. (**A**) miR-29a was downregulated in cervical cancer tissues versus corresponding paracancerous tissues. (**B**) Kaplan–Meier method elucidated low ex[illegible] of miR-2[illegible] predicted poor overall survival. (**C**) The expression of miR-29a was downregulation in HeLa cells than Ect1/E6E7 cells. (**D**) The transfection efficien[illegible] of trans[illegible]ting miR[illegible]a mimic and miR-29a inhibitor in HeLa cells. *P<0.05; **P<0.01.

The mRNA levels of SIRT1 were e[illegible]luate[illegible]er transfected with the miR-29a mimic or [illegible]miR-29a in[illegible]bitor in HeLa cells. As expected, the mRNA l[illegible]el of SIRT1 was inhibited by miR-29a m[illegible]ic (P<0.05), [illegible]while it was enhanced by miR-29a [illegible]nhibitor in HeLa cells (P<0.05) (Figure 3C). Also, the [illegible]otei[illegible]level of SIRT1 was calculated by Western [illegible] and [illegible] found [illegible]e same results with that of mRN[illegible]level, a[illegible] shown [illegible]igure 3D. All the results suggested t[illegible] SIR[illegible]ediated by miR-29a in HeLa cells.

Upregulation of SIRT1 predicted poor prognosis of cervical cancer patients

RT-qPCR assay indicated that SIRT1 was overexpressed in cervical cancer compared to the paracancerous tissues (P<0.05) (Figure 4A). RT-qPCR was employed to assess the expression of SIRT1 in cell lines, and we discovered that SIRT1 was overexpressed in HeLa cells than cervical immortalized squamous cells Ect1/E6E7 (P<0.01) (Figure 4B). Kaplan–Meier method revealed that upregulation of SIRT1 was associated with poor overall survival of cervical cancer patients (P<0.05) (Figure 4C).

SIRT1 reversed partial functions of miR-29a

To verify the functions of SIRT1 in miR-29a overexpressed cells, we re-transfected pcDNA3.1-SIRT1 plasmid into miR-29a overexpressed HeLa cells and RT-qPCR was applied to calculate the transfection efficiency (P<0.05) (Figure 5A). In addition, Transwell assays were conducted to assess the migratory and invasive abilities in HeLa cells. In comparison with cells that only transfected with miR-29a mimic, the migratory and invasive abilities were increased when re-transfected SIRT1 in miR-29a overexpressed cells (P<0.05) (Figure 5B). Upregulation of SIRT1 suppressed E-cadherin expression, and promoted N-cadherin expression in HeLa cells (Figure 5C), which demonstrated that SIRT1 could reverse partial functions of miR-29a on the migratory, invasive and EMT capacities in HeLa cells.

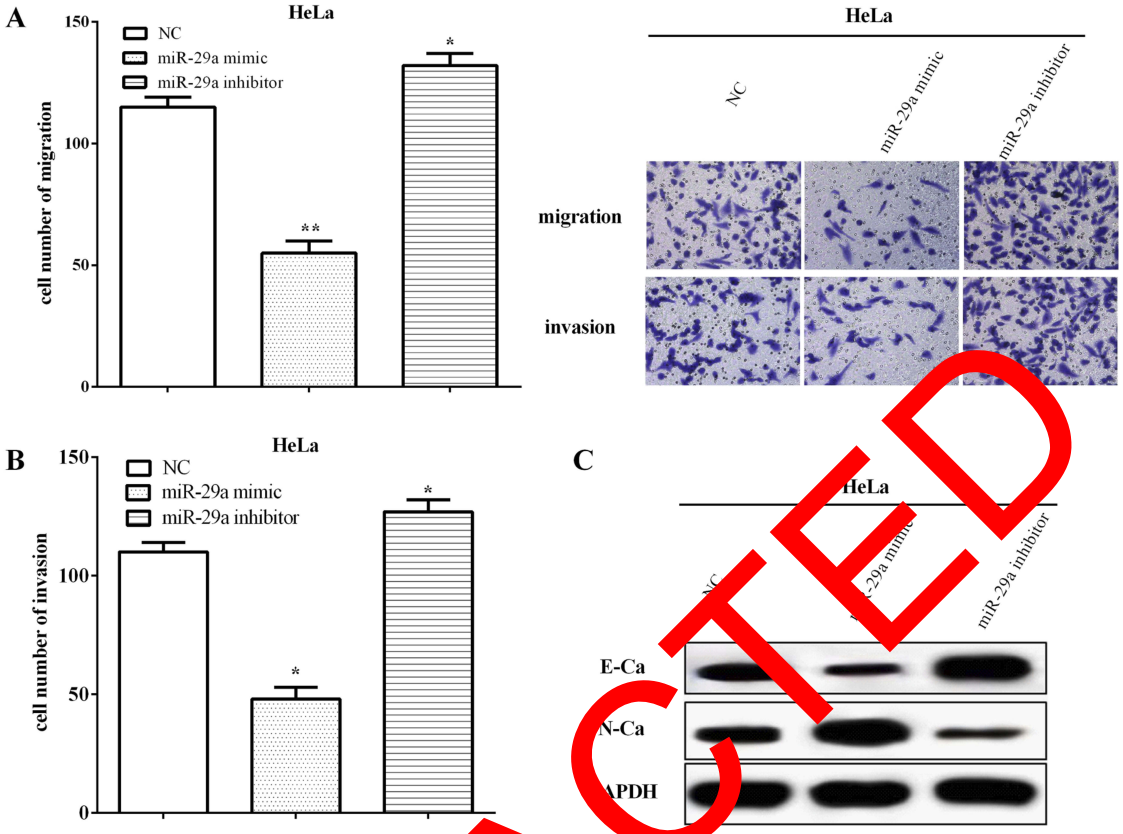

Figure 2 miR-29a impaired cell metastasis and EMT of HeLa cells. (**A**) The miR-29a mimic inhibited the migratory capacity, whereas it was inhibited by the miR-29a inhibitor. (**B**) miR-29a regulated cell invasion in HeLa cells. (**C**) The miR-29a mimic suppressed the expression of E-cadherin while improved the expression of N-cadherin. Meanwhile, the miR-29a inhibitor enhanced the expression of E-cadherin whereas suppressed the expression of N-cadherin. *Compared with NC, $P<0.05$; **Compared with NC, $P<0.01$.
Abbreviations: GAPDH, glyceraldehyde 3-phosphate dehydrogenase; EMT, epithelial–mesenchymal transition; NC, negative control.

Discussion

Cervical cancer is the second most common cause of tumor death in female worldwide with approximately 500,000 new cases of cervical cancer diagnosed each year, of which 280,000 are dead.[19] However, the molecular mechanisms of the development and metastasis of cervical cancer have not been fully elucidated.

MiRNAs, ubiquitous in eukaryotes, are non-coding small RNAs that mediated the expression of target genes by inhibiting transcription or degradation of the mRNA.[20,21] MiR-29a was low expression and inhibited tumorigenesis in multiple cancers, including papillary thyroid carcinoma, colorectal cancer, glioma and pancreatic cancer.[22–25] Su et al[26] indicated that miR-29a inhibited laryngocarcinoma growth by targeting prominin 1. Consistent with the findings of Zamani,[27] we revealed that miR-29a was low expressed in cervical cancer tissues and cell lines, and downregulation of miR-29a was associated with poor outcome of cervical cancer patients. MiR-29a has been reported to act as a tumor suppressor and inhibited the proliferation and metastasis in non-small cell lung cancer.[28] MiR-29a impaired cell viability, migration and invasion and induced the apoptosis of retinoblastoma.[29] Similarly, findings were elucidated in hepatocellular carcinoma, miR-29a suppressed the growth and migration via IGF1R.[30] Our results were consistent with all the findings, miR-29a impaired the metastasis and EMT of cervical cancer cells. Zhang et al[31] elucidated that miR-29a suppressed cell proliferation and cell colony formation by directly binding to SIRT1 in hepatocellular carcinoma. Consistent with Zhang et al,[31] we discovered that SIRT1 was a direct target gene of miR-29a and miR-29a regulated its expression in HeLa cells.

SIRT1 has been reported to act as oncogene and promoted tumorigenesis in a class of cancers, including bladder cancer, angiosarcoma, gastric cancer and renal adenocarcinoma.[32–35] In diabetic conditions, inhibition of SIRT1 induced early calcification and led to cellular senescence of vascular smooth muscle cells.[36] What is more, SIRT1 enhanced the proliferation and differentiation of osteoblast.[37] Consistent with all the findings, we discovered that SIRT1 was upregulated in cervical cancer tissues and cell lines in comparison with the non-

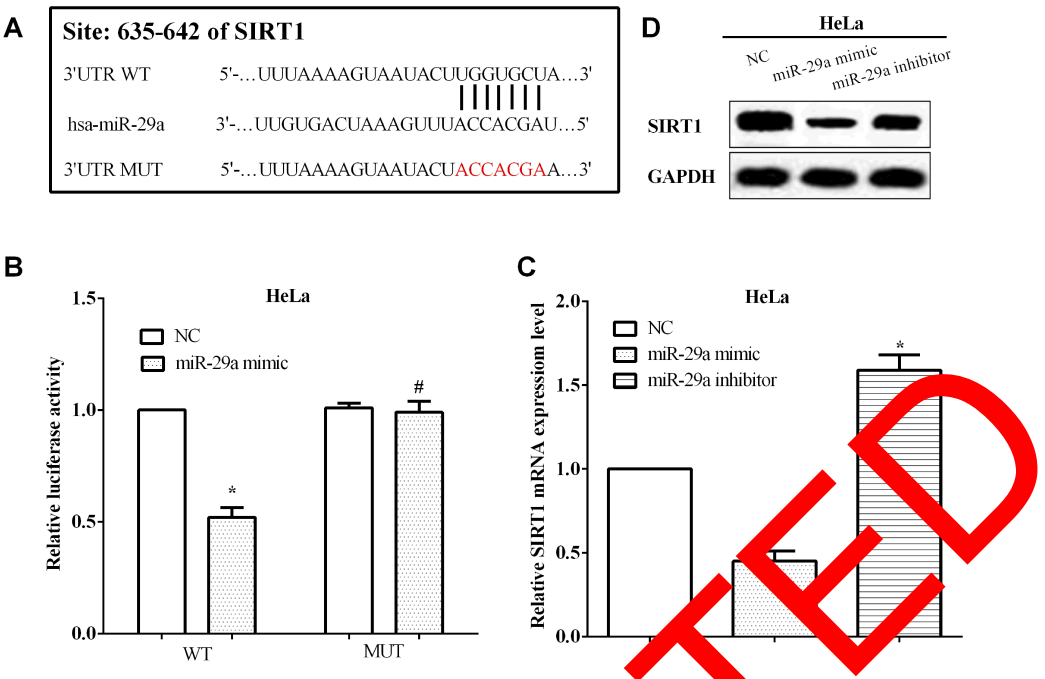

Figure 3 miR-29a regulated the expression of SIRT1 through directly binding to the 3'-UTR of its mRNA. (**A**) TargetScan predicts SIRT1 was a potential target gene of miR-29a. (**B**) The miR-29a mimic inhibited the luciferase activity of cells that transfected wild-type SIRT1 3'-UTR. (**C**) The mRNA level of SIRT1 was inhibited by the miR-29a mimic, while that was enhanced by the miR-29a inhibitor in HeLa cells. (**D**) The protein level of SIRT1 was regulated by miR-29a in HeLa cells. *Compared with NC, $P<0.05$; #Compared with NC, $P>0.05$.

Abbreviations: SIRT1, Sirtuin-1; 3'-UTR, 3'-untranslated region; WT, wild type; MUT, mutant; NC, negative control.

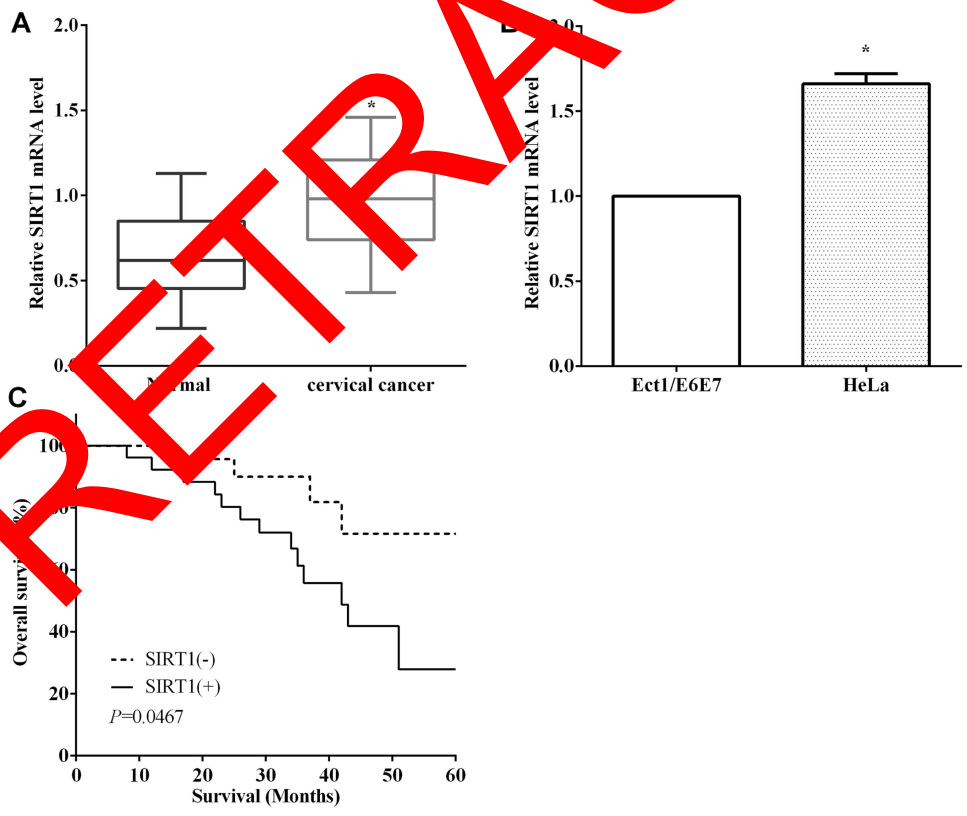

Figure 4 Upregulation of SIRT1 predicted poor prognosis of cervical cancer patients. (**A**) SIRT1 was overexpressed in cervical cancer tissue compared to the normal tissues. (**B**) SIRT1 was overexpressed in HeLa cells than cervical immortalized squamous cells Ect1/E6E7. (**C**) Upregulation of SIRT1 was associated with poor overall survival of cervical cancer patients.*$P<0.05$.

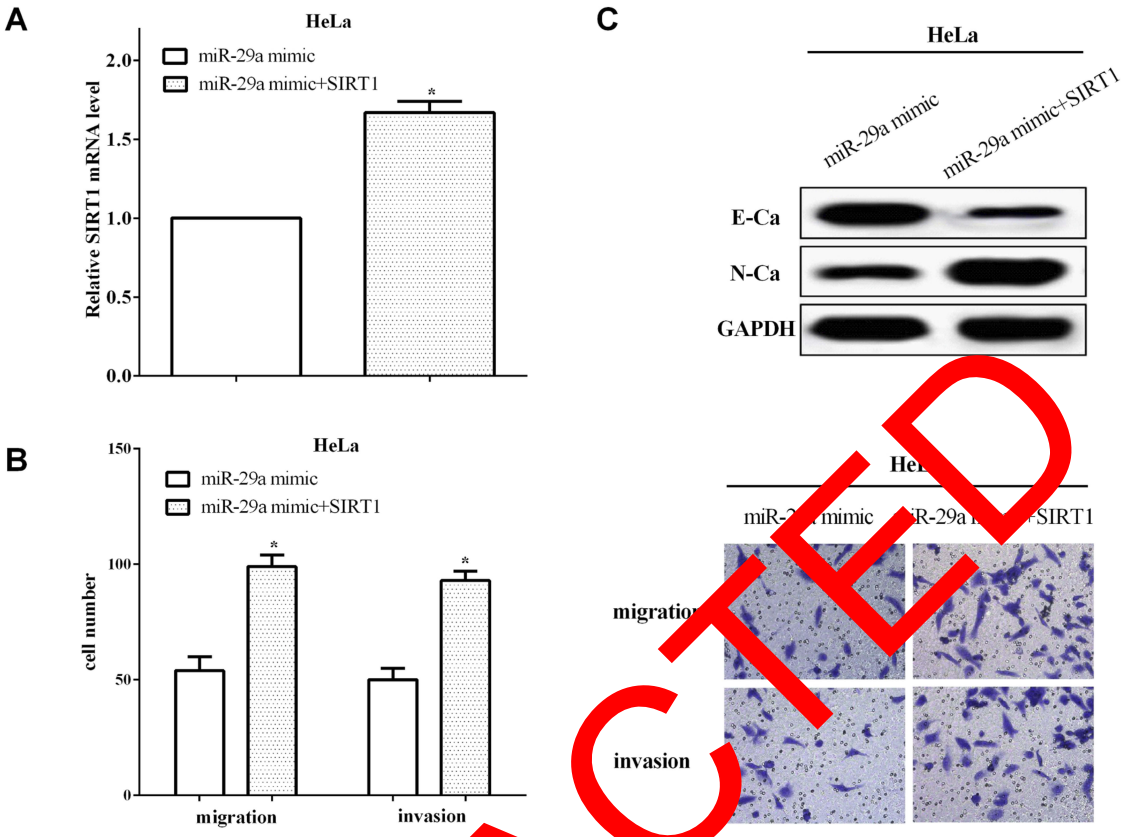

Figure 5 SIRT1 reversed partial functions of miR-29a. (**A**) The transfection efficiency was calculated of re-transfecting pcDNA3.1-SIRT1 plasmid in miR-29a overexpressed HeLa cells. (**B**) The migratory and invasive abilities were increased when re-transfected SIRT1 in miR-29a overexpressed cells. (**C**) SIRT1 could reverse partial functions of miR-29a on the EMT capacity in HeLa cells. *P<0.05.

Abbreviations: SIRT1, Sirtuin-1; GAPDH, glyceraldehyde phosphate dehydrogenase; EMT, epithelial–mesenchymal transition.

tumor tissues and normal cell lines. Upregulation of SIRT1 predicted worse outcome of cervical cancer patients. Knockdown of SIRT1 inhibited the migratory and invasive abilities of colorectal cancer.[38] Our findings were in accordant with all the previous findings, and we discovered miR-29a was participated in the migration, invasion and EMT in cervical cancer through targeting SIRT1. SIRT1 reversed the partial roles of miR-29a on metastasis.

Conclusion

MiR-29a was low expressed in cervical cancer and downregulation of miR-29a was associated with poor outcome. MiR-29a regulated the expression of SIRT1 by directly targeting to its 3'-UTR of mRNA in HeLa cells. SIRT1 was upregulated in cervical cancer tissues and cell lines in comparison with the non-tumor tissues and normal cells. Upregulation of SIRT1 predicted worse outcome of cervical cancer patients. MiR-29a participated in the migration, invasion and EMT in cervical cancer through directly targeting to 3'-UTR of SIRT1 mRNA. SIRT1 reversed partial roles of miR-29a on migration, invasion and EMT.

Disclosure

The authors report no conflicts of interest in this work.

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